

&lt;!--StartFragment--&gt;RESULT 5

ABB75752

ID ABB75752 standard; protein; 708 AA.

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AC ABB75752;

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DT 15-JUN-2007 (revised)

DT 24-JUN-2002 (first entry)

XX

DE Human gp354 (putative splice variant).

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KW Human; GP354; immunoglobulin; pancreas; central nervous system;

KW diagnosis; gene therapy; pancreatitis; inflammation; tumour; cancer;

KW autoimmune disease; Alzheimer's disease; Parkinson's disease;

KW senile dementia; migraine; epilepsy; neurasthenia; neuropathy;

KW neural degeneration; antiinflammatory; cytostatic; nootropic;

KW immunosuppressive; antiparkinsonian; neuroprotective; antimigraine;

KW anticonvulsant; splice variant; BOND\_PC; LRMR5827;

KW LRMR5827 [Homo sapiens]; GO7155; GO16020; GO16021.

XX

OS Homo sapiens.

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FH Key Location/Qualifiers

FT Peptide 1. .21

FT /label= Signal\_peptide

FT Protein 22. .708

FT /label= Mature\_protein

FT Domain 22. .510

FT /note= "extracellular domain"

FT Domain 38. .109

FT /note= "Ig domain"

FT Domain 139. .206

FT /note= "Ig domain"

FT Domain 242. .293

FT /note= "Ig domain"

FT Domain 326. .377

FT /note= "Ig domain"

FT Domain 413. .488

FT /note= "Ig domain"

FT Domain 511. .533

FT /note= "transmembrane domain"

FT Domain 534. .708

FT /note= "intracellular domain"

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PN WO200198360-A2.

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PD 27-DEC-2001.

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PF 22-JUN-2001; 2001WO-US019904.

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PR 22-JUN-2000; 2000US-0213611P.

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PA (BIOJ ) BIOGEN INC.

PA (CARU/) CARULLI J P.

PA (LUKA/) LUKASHIN A V.

PA (KILB/) KILBURN D R.

PA (SUNC/) SUN C.

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PI Carulli JP, Lukashin AV, Kilburn DR, Sun C;

XX

DR WPI; 2002-329171/36.

Query Match 85.6%; Score 3156.5; DB 5; Length 708;  
Best Local Similarity 84.3%; Pred. No. 2.7e-212;  
Matches 594; Conservative 40; Mismatches 66; Indels 5; Gaps 2;

Qy	1	MLASALLVFLCCFKGHAGSSPHFLQQPEDMVVLGEEARLPCALGAYRGLVQWTKDGLAL	60
		:                 :	
Db	4	MRVPALLVLLFCFRGRAGSPHFLQQPEDLVVLGEEARLPCALGAYWGLVQWTKSGLAL	63
Qy	61	GGERDLPGWSRYWISGNSASGQHDLHIKPVELEDEASYEQASQAGLRSRPAQLHVMVPP	120
		:                     :   :           :                     :	
Db	64	GGQRDLPGWSRYWISGNAANGQHDLHIRPVELEDEASYEQATQAGLRSRPAQLHVLVPP	123
Qy	121	EAPQVLGGPSVSLVAGVPGNLTCSRSGDSRPAPPELLWFRDGIRLDASSFHQTTLKDKATG	180
		:               :     :           :	
Db	124	EAPQVLGGPSVSLVAGVPANLTCSRSGDARPTPELLWFRDGVLLDGATFHTLLKEGTPG	183
Qy	181	TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTLSLQYPPMVTLSAEPQTVQEGEK	240
		:     :                 :                 :	
Db	184	SVESTLTLPFSHDDGATFVCRARSQLPTGRDTAITLSLQYPEVTLSASPHTVQEGEK	243
Qy	241	VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADATFLTEPVSCEVSNVAGSANRS	300
		:	
Db	244	VIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADASFLTEPVSCEVSNVAGSANRS	303

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